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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 08:17:51 2000; MasPar time 22.33 Seconds 662.959 Million cell updates/sec

Title:

Description:
Perfect Score:
Sequence: >US-09-331-631-5 (1-625) from US09331631.pep (1 of 4) 4631 1 QCMQLETSGQMRRCVSQCDK.....SPRSTKQQQPLVSILDFVGF 625

Scoring table: PAM 150 Gap 11

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 36.852; Variance 168.946; scale 0.218

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118 2322118 242210		Result No.
11149 1073 1004 1092 992 972 930 920 920 920 930 128 826 128 128 128 128	4631 4496 4487 1302	Score
224 222 222 222 222 222 222 222 222 222		Query Match
. 4 6 4 6 5 5 5 6 6 1 4 6 6 5 6 5 6 6 1 4 6 6 6 1 4 6 6 6 1 4 6 6 6 1 4 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6 6 1 6	3 U O O O U I	Length
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Theobroma cacao antimi Zea mays antimicrobial G. max SBP2 protein. G. max SBP2 protein. G. max sBP1 protein. Glycine max antimicrob G. max truncated SBP1 Peanut allergen Ara hi Peanut allergen Ara hi Arachis hypogaea antimi Mouse SRY-related prot Trypanosoma cruzi anti Dirofilaria immitis pa Human regulatory molec Mammalian Ena (Mena). Mouse neural Mena+ pro Mouse neural Mena+ pro	Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Sequence encoded by 67	Description
3.30e 91 3.30e 84 3.38e 84 3.38e 81 1.04e 76 2.13e 71 4.06e 70 4.06e 70 5.13e 68 5.13e 68 5.13e 68 5.13e 60 1.53e 01 1.53e 01 5.15e 01 5.15e 01 5.15e 01	n w o o o	Pred. No.

	W31949	μ,	3801	2.2	103	45
Human bg protein	W31950	Н	3672	2.2	103	44
Mouse metastasis-assoc	W31866	ب	1343	2.2	104	43
70K autoantigen, part	R82630		614	2.3	108	42
Leucocytozoan protozoa	R70491	-ب	562	2.3	106	41
Renal cancer associate	Y07067	Н	482	2.3	106	40
Human 70K Ul snRNP pro	W03662	سا	436	2.3	108	39
Sequence of Histidine-	R24393	۳	351	2.3	105	38
E. coli RNase E.	R82664	۳	190	2.3	107	37
Escherichia coli	W94681	ш	190	2.3	107	36
Mannose-1-phosphate tr	W30763	щ	1178		111	35
Human secreted protein	W74802	Ь	521		109	34
HTLV-1 protein express	R12844	بــ ـا	265	2.4	110	33
Staphylococcus aureus	W89768	Н	167	2.4	110	32
Zea mays antimicrobial	W62836	ب	33		109	31
CORK potassium channel	R97985	سا	1529		115	30
Stenocarpus sinuatus	W62841	_	28	2.6	119	29
Human metastasis-assoc	W31867	ب	1382		124	28
-	W88788		567		124	27
P.falciparum LSA gene	R26944	μ	493	•	127	26
P.falciparum LSA-R-NR	R26941	۲	316	2.7	127	25
Mouse neural Mena+++	W37153	Ц	802	2.8	128	24

ALIGNMENTS

Оy	δ. β.	ОУ	Db Оу	Ma Be	SS	ဂ္ဂ	38	PS -	i i	DR	DR I	PA	PR	PΕ	יי כל	H	ΗŢ	ΗŢ	FT:	ין ע	S S	DE	당 ?	BB	RESULT
181 QHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSK 240 	121 QKRYEEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQR 180 	61 CORRCKEICEEEEEYNRORDPQQOYEQCOKRCQRRETEPRHMQICQQRCERRYEKEKRKQ 120 	1 QCMQLETSGOMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESDPRQQQY 60	Query Match 100.0%; Score 4631; DB 1; Length 625; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 625 AA;	imals.	The sequence is that of an antimicrobial protein which can be used to control microbial infectations in plants and mammalian	Claim 1; Page 43-45; 96pp; English.	Novel anti-microbial protein from e.g. Macadamia integrifolia -	N-PSDB; V42316.	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP; wPI: 98-377279/32.		1996;	22-DEC-1997; AU0874.	02-JHI-1998	/note= "mature protein"			Peptide 128	addiita Integr	bial protein; infestation; c	Macadamia integrifolia antimicrobial protein.	27-OCT-1998 (first entry)	W62830 standard; Protein; 625 AA.	LT 1

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The sequence is that of an antimicrobial protein which
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20-DEC-1996; AU-004275.
(RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.
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WPI; 98-377279/32.
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                                                                                                                                  Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1; Page 34-36; 96pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and be used to control microbial infestations in plants and
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Key

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20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY BOWER NI, GOULTER KC, Green JL, Manners JM, May WPI: 98-377279/32.
N-PSDB; V42310.
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Claim 4; Fig 2; 59pp; English.

The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1991; G00914.
11-JUN-1999; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin E,
WPI: 92-024418/03.
N-PSDB; Q20377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1992 (first entry)
Sequence encoded by 67 kD
Cocoa; flavour; vicilin; s
                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant cocoa proteins - beans and produced in large of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9119801-A.
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    are responsible for flavour in cocoa
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Pred. No. 3.01e-105;
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Best Local Similarity
Matches 225; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gossypium hirsutum antimicrobial protein.
antimicrobial protein; infestation; control
Gossypium hirsutum.
W09827805-A1.
02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOL
Bower NI, Goulter KC, Green JL, Manners JM,
WPI; 98-377779/32.
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W62832;
27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                     Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of Claim 1; Page 49-51; 96pp; English.

The sequence is that of an antimicrobial protein
                                                                                                                                                                                                                                                                                                 Sequence
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LLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTP
                                                                                                DPQQQYEQCQKRCQRRETEPRHMQICQQRCERRY-EKEK--R-K-Q--QKRYEE-QQ--R
                                                                                                                             DPPKRYEDCKRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR
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  EDEEK--
                                               QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN 155
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llarity 39.9%;
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                                                                                                                                                                                            Score 1244; DB 1;
Pred. No. 6.82e-100;
149; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                   infestations
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                             Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1, Page 47-49; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
                                                                                                                                                                                                                                                        animals.
Sequence
                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWET NI, GOULTEY KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                Theobroma cacao. WO9827805-A1.
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27-OCT-1998 (first entry)
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                                                                                                                                                                                                   Match 24.8%; Local Similarity 40.4%; es 193; Conservative
                                                                                                                                             YFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGSTVYVVSQDNQEKLTIAVLALPVNSP
                                                      FPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPNTFILPHHCDAEAI
                                                                                       DCRRHC-EQQE-PRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYY 212
                                                                                                          QCQGRCQEQQQGQREQQQCQRKCWEQYKEQERG-EHENYHNHKKNRSEEEEGQQRNNPYY 145
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 <del>--</del>
                                                                                                                                                                                                                                                        525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
 ::<del>-</del>::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525
                                                                                                                                                                                                   Score 1149; DB 1; I
Pred. No. 3.90e-91;
121; Mismatches 141;
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22-DEC-1997; I
20-DEC-1996; I
(RETR-) COOP I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 58-60; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal be used to control microbial infestations in plants.
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20-DEC-1996: AU-004275.
20-DECTP96: AU-004275.
(RETR-) COOP RES CENT TROPICAL |
BOWET NI, GGulter KC, Green JL,
WPI; 98-377279/32.
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27-0CT-1998 (first entry)
Zea mays antimicrobial protein
antimicrobial protein; infestation;
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WO9827805-Al.
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                                    SQGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVAS 442
                                                                                                                                                QLYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVCPHRQ
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Pred. No. 3.83e-84;
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Claim 13b; Page 37-38; 58pp; English.
This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.
The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content
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22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI; 99-070155/06.
New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in developing seeds and so may be used to express any transgene in developing seeds.
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                                                              QRLNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSR----SDSK-HD
                                                                                                                               ASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%; Score 1041; DB 1; larity 36.7%; Pred. No. 3.33e-81; Conservative 135; Mismatches 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developing seeds.
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Best Local Similarity 37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified amino acid sequence compared to a corresponding wiid-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wiid-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity, particularly in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Page 34-36; 58pp; English.
This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds pisclosure; Page 34-36; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON Chao WS, Grimes HD; WPI; 99-070155/06.
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21-MAY-1998; U10465.
22-MAY-1997; US-047568
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WO9853086-A1.
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24-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                              FDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVNRDENDKLFLAMLH
                          QRLNLMLTFTNITQRSMSTIHYNSHATKIALVIDGRGHLQISCPHMSSR-SSHS--K-HD
                                                                                                                                                                                                                          LQ-TISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVLGQQREGVIIRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQREY-EDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGG-DLMNPQRGGSGRYEEGEEKQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQYTEGDKRVCLQSCDRYHRMKQER-EKQIQEETREKKEEESREREEEQQ-EQHEE-Q 105
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                                                                                             SQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDY-RQ-L
                                                                                                                                                             SREQVRALAPTKKSSW-WPF--GGES-KPQFNIFSKRPTISNGYGRLTEVGPDDDEKSWL
                                                                                                                                                                                                                                                                                         IPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQAALQTPKGKLENVFDQQNEGSIFRI 285
                                                                                                                                                                                                                                                                                                                                                             LDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTH
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; Pred. No. 1.04e-76;
125; Mismator
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Best Local S
Matches 19
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(REIR-) COOP RES CENT TROPICA
Bower NI, Goulter KC, Green J
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for controlling microbial infestations of plants claim 1; Page 63-65; 95pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or mammals
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Glycine max antimicrobial protein.
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W62838;
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RNVLQQIEPQAMELAFAASRKEVEELF
QVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEP
                                                                                                                                                                                                            TEAQQSYLQGFSRNILEASYDTKFEEINKVLFSREEGQQQGEQRLQESVIVEISKEQIRA 386
                                                                                                                                                                                                                                                                                       SLVNNDDRDSYRLQSGDALRVPSGTTYYVVNPDNNENLRLITLAIPVNKPGRFESFFLSS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQRRCRQQESDPRQQQYCQRRCKEICEEEEEEYNRQRDPQQQYEQCQKRCQRRETEPRHMQ 103
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                                                            IVDMNEGALLLPHFNSKAIVILVINEGDANIELV-G-LKEQQQEQ---QQEEQPLEVR--
                                                                                                                        LT-RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVF
                                                                                                                                                        LSKRAKSSSRK-TI--SSED-K-PFNLRSRDPIYSNKLGKFFEITPEKNPQLRDLDIFLS 441
                                                                                                                                                                                          GQNPEPYLSTFSKEILEAALNTQ-TE--R-L--R--GVL-GQQR--EGVIIRASQEQIRE
                                                                                                                                                                                                                                                        KMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAG
                                                                                                                                                                                                                                                                                                                         FRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGAL 281
                                                                                                                                                                                                                                                                                                                                                      FKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNSKPNTLLLPNHADADYLIVILNGTAIL 266
                                                                                                                                                                                                                                                                                                                                                                                         EPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGE-EKQSD-NPYYFDERSLSTR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDEDE-QPR-PIPFPRPQPR-QEEEHEQREE-QEWPRK-EEKRGEKGSEEED-EDEDEEQ 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDMDVSVFIANITQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRGGGKRHE
                              KYRAELSEQDIFVIPAGYPVV-VNATS-NLNFFAIGINAENNQRNFLAGSQDNVISQIPS 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEEEVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENF-LAGRE 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TROPICAL PLANT PATHOLOGY Green JL, Manners JM, Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 972; DB 1; Length 605
Pred. No. 7.08e-75;
162; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587
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569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a novel sucrose binding protein, SBP1 isolated CC from Glychne max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a CC modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers cenhanced sucrose uptake compared to the corresponding wild-type SBP.

CC Products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing confers seeds. Enhanced sucrose uptake activity in developing seeds may be constable where it is an advantage to increase the carrobhydrate content of the seed (e.g. where the seed is the primary plant material harvested, contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is contrasted. The SBP regulatory regions confer specific or enhanced correspond in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G. max truncated SBP1 protein. SBP1; sucrose binding protein; SBP2. seed; carbohydrate content; soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds claim 7; Page 36-37; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chao WS, Grimes H
WPI; 99-070155/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9853086-A1.
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                                                       SREQVRALAPTKKSSW-WPF--GGES-KPQFNIFSKRPTISNGYGRLTEVGPDDDEKSWL
                                                                                                                                                                                                           QAMELAFAASRKEVEELFNSQDESIFFPGPRQHQQQSPRSTKQQQPLVSIL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKG--PLSSIL
                                                                                                                                                                                                                                                                                       EDSEVVEFNIKGRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVNRDENDKLFLAMLH
                                                                                                                                                                                                                                                                                                                                                                                   DENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPRH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQQQYTEGDKRVCLQSCDRYHRMKQER-EKQIQEETREKKEEESREREEEQQ-EQHEE-Q 105
                                   QDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGGKRHE
                                                                                                             SQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDY-RQ-L
                                                                                                                                                                                       LQ-TISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVLGQQREGVIIRA
                                                                                                                                                                                                                                                                     LDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF-
                                                                                                                                                                                                                                                                                                                                                 SDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTH
                                                                                                                                                                                                                                                                                                                                                                                                                           QQREY-EDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGG-DLMNPQRGGSGRYEEGEEKQ
KSSPS-YHRISSDLKPGMVFVVPPGHPFVTIASNKENLLMICFEVNAR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
156; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 934; DB 1; Length 444;
; Pred. No. 2.13e-71;
112; Mismatches 121; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peanut allergens Ara hI and Ara hII - used for vaccination and in two-site monoclonal antibody based ELISA
SC Claim 31; Page 172; 354pp; English.
This polypeptide comprises major peanut allergen Ara hI (W22149).
Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut C hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site C MAD ELISA for the detection of Ara hI or Ara hII (claimed). Ige-to binding Ara hI antigen epicopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens,
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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Bannon GA, Burks AW,
WPI: 97-363453/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hI. Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1997 (first entry)
Peanut allergen Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W22150 standard; Protein; W22150;
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29-DEC-1995; US-009455.
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 373
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                                                                                                                                                                                                                                                                                                                           .78
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                              QPRREEGG-RWGPAGPRE-RE-REE-DWRQPREDWR--RPSHQQPRKIRPEGREGEQEWG 159
                                                                           DNQNLRVAKISMPVTQPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLE
                                                                                                                                              AKPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRH
                                                                                                                                                                                              GSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLE
                                                                                                                                                                                                                        TPGSHVR-EETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIE 218
                                                                                                                                                                                                                                                                                                                                                 QQEPDDLKQKACESRCTKLEYDPRCVYDPRGHTGTTNQRSPPGERTR-GRQPGDYDDDRR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anaphylactic shock.
                              ENAGGEQEERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSVSKKGSEEEGDITNPI
                                                            NNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGYL--
                                                                                                                             ANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRD
                                                                                                                                                                                                                                                             EERMKEGDNKRDPQ-QREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRG
                                                                                                                                                                                                                                                                                                                             QRDPQQQYEQ-CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQRE-DEEKY 135
                                                                                                                                                                                                                                                                                                                                                                                            190;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
-GVI---IRASQE-Q--IRELTRDD-SE-SRR-WHI-RRGGE--SS-RGPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            19.9%;
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                                                                                                                                                                                                                                                                                                                                                                                              153;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 920; DB 1;
Pred. No. 4.06e-70;
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 626
                                                                                                                                                                                                                                                                                                                                                                                              Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                            338
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414
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HRESULT PRESCRIPTOR WAS SEEN ACCORDED TO SEEN ACCORDED TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uptake activity in developing seeds
Claim 7: Page 39-40; 58pp; English.
This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.
The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity, particularly in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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21-MAY-1998, U10465.
22-MAY-1997, US-047568.
(UNIW ) UNIV WASHINGTON S
Chao WS, Grimes HD;
WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max. WO9853086-A1.
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SBP1; sucrose binding protein; SBP2;
seed; carbohydrate content; soybean.
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W90342;
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      323
                                                                                                                        263
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                                                                                                                                                                                                                                                                                                                                                                      149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 19.6%;
Local Similarity 38.8%;
                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                                                                                                                                                                                                            KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVLGQQREGVIIR
                                                                                                                                                    PRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDENEKLLLA
                                                                                                                                                                                                                                       EKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL
                                                                                                                                                                                                                                                                             EEEDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVS 151
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                                                         MLHIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFNQQNEGSIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKESHFVSARPQSQSQSPSSPEKESP 602
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                                                                                                                        PTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 907; DB 1;
Pred. No. 6.27e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 409;
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                                                                                                                                                                                                                                                                                                  This polypeptide comprises major peanut allergen Ara hI (W22149).

CITE sequence was deduced from CDNA clone P17 (T76612), isolated from peanut seed cDNA using a primer (see T76612), isolated from peanut seed cDNA using a primer (see T7661) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum ig from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1997.
23-SEP-1996;
04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peanut allergen Ara hI.
Peanut; seed storage protein; allergen
vaccine; anaphylactic shock; immunothe
monoclonal antibody; ELISA; analysis;
Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peanut allergens Ara hI and Ara hII - two-site monoclonal antibody based ELI Claim 31; Page 169; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 97-363453/33.
N-PSDB; T76612.
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Bannon GA, Burks AW,
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256
256
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                          RPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHD 273
NPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDN
                                                                           PGS-EVREETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQIEA
                                                                                                                    ERMKEGDNKRDP-QQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGG 195
                                                                                                                                       PRREEGG-RWGPAEPRE-RE-REE-DWRQPREDWR--RPSHQQPRKIRPEGREGEQEWGT 154
                                                                                                                                                                               QRDPQQQYEQ-CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYE
                                                                                                                                                                                                           QQEPDDLKQKACESRCTKLEYDPRCVYDTGAT-NQRHPPGERTRG-R-QPGDYDDDRR-Q 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGR 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | CRENEMETETNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRSDSK 380
                                                                                                                                                                                                                                            191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burks AW, Cockrell G,
                                                                                                                                                                                                                                         19.4%;
larity 33.8%;
Conservative
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US-009455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylation
                                                                                                                                                                                                                                         Score 897; DB 1;
Pred. No. 5.13e-68;
157; Mismatches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; allergen; allergy; hypersensitivity;
immunotherapy; therapy;
analysis; Ara hI.
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                                                                                                                                                                                                                                                                       Length 614;
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 191; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1998.
02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for controlling microbial infestations of plants claim 1; Page 55-57; 96pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W62834;
W62834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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334 NAGGEQEERGQRRRSTRSSDNEGVIVKVSKEHVQELTKHAKSVSKKGSEEEDITNPINLR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572
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                                                                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 PRREEGG-RWGPAEPRE-RE-REE-DWRQPREDWR--RPSHQQPRKIRPEGREGEQEWGT
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                                                                                                                                                                                                                                                                                                                                                      PGS-EVREETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQIEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRDPQQQYEQ-CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRES-HFVSARPQSQSPSSPEKEDQ 595
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                                                                                    NERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL---
                                                                                                                                              NONLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEE
                                                                                                                                                                                                        NPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDN
                                                                                                                                                                                                                                                                                                                        SGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GVI---IRASQEQ--IRELTRDDS-E-SRR-WHI-RRGGES-S-RGPYNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 897; DB 1;
Pred. No. 5.13e-68;
157; Mismatches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from e.g. Macadamia integrifolia -
pial infestations of plants or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control.
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